

In the Claims

1. (currently amended) A method of predicting whether a subject will be susceptible to undesirable toxicity resulting from treatment with an anti-proliferative therapy, said method comprising:

(a) obtaining an expression profile for ~~any gene from Table 3 at least 10 sequences selected from the 50 top ranked genes set forth in Table 3~~ for a response to said anti-proliferative therapy in a sample from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to predict whether said subject is susceptible to undesirable toxicity.

2. (original) The method according to Claim 1, wherein said anti-proliferative therapy comprises administration of ionizing radiation.

3. (original) The method according to Claim 1, wherein said anti-proliferative therapy comprises administration of a chemotherapeutic agent that results in DNA damage.

4. (original) The method according to Claim 3, wherein said DNA damage comprises double-stranded breaks in DNA.

5. (currently amended) A method of determining whether a subject is susceptible to undesirable toxicity resulting from treatment with radiation therapy, said method comprising:

(a) obtaining an expression profile for the response to radiation for a sample for ~~any gene from Table 3 at least 10 sequences selected from the 50 top ranked genes set forth in Table 3~~ from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine whether said subject is susceptible to undesirable radiation toxicity.

6. (original) The method according to Claim 5, wherein expression profile is a transcriptional profile.

7. (canceled)

8. (currently amended) The method according to Claim 5, wherein said expression profile comprises at least 50 25 sequences from Table 3 selected from the 50 top ranked genes set forth in Table 3.

9. (original) The method according to Claim 5, wherein said undesirable toxicity is at least a grade 2 toxicity.

10. (currently amended) A method of determining whether a subject is susceptible to undesirable toxicity resulting from treatment with administration of a chemotherapeutic agent that induces double-stranded breaks in DNA, said method comprising:

(a) obtaining an expression profile for the response to said chemotherapeutic agent for a sample for any gene from Table 3 at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine whether said subject is susceptible to undesirable toxicity.

11. (currently amended) A method of predicting whether a subject will be susceptible to undesirable toxicity resulting from treatment with radiation therapy, said method comprising:

(a) obtaining an expression profile for the response to radiation for a sample for any gene from Table 3 at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine the probability that said subject is susceptible to undesirable radiation toxicity.

12. (original) The method according to Claim 11, wherein expression profile is a transcriptional profile.

13. (canceled)

14. (currently amended) The method according to Claim 11, wherein said expression profile comprises at least 50 25 sequences from Table 3 selected from the 50 top ranked genes set forth in Table 3.

15. (original) The method according to Claim 11, wherein said undesirable toxicity is at least a grade 2 toxicity.

16. (canceled)

17. (currently amended) A method of determining the suitability of a patient for radiation therapy, the method comprising:

predicting whether a subject will be susceptible to undesirable toxicity resulting from treatment with radiation therapy, said method comprising:

(a) obtaining an expression profile for the response to radiation for a sample for any gene from Table3 at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine the probability that said patient is susceptible to undesirable radiation toxicity;

wherein a patient that is predicted to have a high probability of undesirable radiation toxicity is less suitable for radiation therapy.

18. (original) The method according to Claim 17, wherein expression profile is a transcriptional profile.

19. (canceled)

20. (currently amended) The method according to Claim 17, wherein said expression profile comprises at least 50 25 sequences from Table3 selected from the 50 top ranked genes set forth in Table 3.

21. (original) The method according to Claim 17, wherein said undesirable toxicity is at least a grade 2 toxicity.

22. (currently amended) A method of determining the suitability of a patient for treatment with an anti-proliferative chemotherapeutic agent that induces double-stranded breaks in DNA, the method comprising:

predicting whether a subject will be susceptible to undesirable toxicity resulting from treatment with said chemotherapeutic agent, said method comprising:

(a) obtaining an expression profile for the response to said chemotherapeutic agent for a sample for ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine the probability that said patient is susceptible to undesirable toxicity;

wherein a patient that is predicted to have a high probability of undesirable toxicity is less suitable for said treatment with an anti-proliferative chemotherapeutic agent.

23. (currently amended) A method of optimizing anti-proliferative therapy for a patient, the method comprising:

(a) obtaining an expression profile for the response to said anti-proliferative therapy for a sample for ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject; and

(b) comparing said obtained expression profile to a reference expression profile to determine the probability that said patient is susceptible to undesirable toxicity;

wherein a dose of said anti-proliferative therapy is selected to minimize to undesirable toxicity, while providing for effective anti-proliferative activity.

24. (original) The method according to Claim 23, further comprising obtaining an expression profile for a response to one or more additional anti-proliferative therapies;

comparing said expression profiles to determine which therapy minimizes undesirable toxicity while providing for effective anti-proliferative activity.

25. (currently amended) The method according to Claim 23, further comprising obtaining an expression profile for the response to said anti-proliferative therapy for (i) a normal cell sample for ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject and (ii) a tumor cell sample ~~any gene from Table 3~~ at least 10 sequences selected from the 50 top ranked genes set forth in Table 3 from said subject;

comparing said expression profiles from said normal cell and said tumor cell to determine which therapy minimizes undesirable toxicity while providing for effective anti-proliferative activity.

26. (currently amended) A method of obtaining an expression profile for the transcriptional response to radiation, the method comprising:

exposing a cell sample from an individual to radiation;

extracting mRNA from said cell;

~~quantitating the level of mRNA corresponding to a sequence in Table 3 at least 10 sequences selected from the 50 top ranked genes set forth in Table 3;~~

comparing said level of mRNA to the level of said mRNA present in a cell sample from said individual not exposed to radiation.

27. (original) The method according to Claim 26, wherein said exposing to radiation comprises exposes said cell to a dose of ionizing radiation of from about 2 to about 10 Gy.

28. (original) The method according to Claim 27, wherein said mRNA is extracted after at least about 2 and not more than about 24 hours following said exposure.

29. (original) The method according to Claim 27, further comprising exposing a cell sample from said individual to ultraviolet radiation at a dose of at least about 5 J/m<sup>2</sup> and not more than about 50 J/m<sup>2</sup>.

30. (original) The method according to Claim 29, wherein said mRNA is extracted after at least about 4 and not more than about 72 hours following said exposure.

31. (original) The method according to Claim 26, wherein said comparing step comprises a nearest shrunken centroid analysis step.

32. (original) A method of obtaining an expression profile for the transcriptional response in a phenotype of interest, the method comprising:

exposing a cell sample from an individual to said anti-proliferative therapy;

extracting mRNA from said cell;

quantitating the level of mRNA corresponding to a sequence of interest;

comparing by nearest shrunken centroid analysis said level of mRNA to the level of said mRNA present in a cell sample from said individual not exposed to said anti-proliferative therapy.

33. (original) The method according to Claim 32, wherein said phenotype of interest comprises anti-proliferative therapy.

34-46 (canceled)